

SEQUENCE LISTING

<110> Hinrichs, Steven H.

<120> Methods and Compositions for Modulation of
Transcription Factor Activity

<130> N1374007

<140>

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<150> 08/210880

<151> 1994-03-18

<150> 08/881800

<151> 1997-06-24

<160> 13

<170> PatentIn Ver. 2.1

<210> 1

<211> 271

<212> PRT

<213> Homo sapiens

<400> 1

Met Glu Asp Ser His Lys Ser Thr Thr Ser Glu Thr Ala Pro Gln Pro
1 5 10 15

Gly Ser Ala Val Gln Gly Ala His Ile Ser His Ile Ala Gln Gln Val
20 25 30

Ser Ser Leu Ser Glu Ser Glu Glu Ser Gln Asp Ser Ser Asp Ser Ile
35 40 45

Gly Ser Ser Gln Lys Ala His Gly Ile Leu Ala Arg Arg Pro Ser Tyr
50 55 60

Arg Lys Ile Leu Lys Asp Leu Ser Ser Glu Asp Thr Arg Gly Arg Lys
65 70 75 80

Gly Asp Gly Glu Asn Ser Gly Val Ser Ala Ala Val Thr Ser Met Ser
85 90 95

Val Pro Thr Pro Ile Tyr Gln Thr Ser Ser Gly Gln Tyr Ile Ala Ile
100 105 110

Ala Pro Asn Gly Ala Leu Gln Leu Ala Ser Pro Gly Thr Asp Gly Val
115 120 125

Gln Gly Leu Gln Thr Leu Thr Met Thr Asn Ser Gly Ser Thr Gln Gln
130 135 140

Gly Thr Thr Ile Leu Gln Tyr Ala Gln Thr Ser Asp Gly Gln Gln Ile
145 150 155 160

Leu Val Pro Ser Asn Gln Val Val Val Gln Thr Ala Ser Gly Asp Met
165 170 175

Gln Thr Tyr Gln Ile Arg Thr Thr Pro Ser Ala Thr Ser Leu Pro Gln
180 185 190

Thr Val Val Met Thr Ser Pro Val Thr Leu Thr Ser Gln Thr Thr Lys
195 200 205

Thr Asp Asp Pro Gln Leu Lys Arg Glu Ile Arg Leu Met Lys Asn Arg
210 215 220

Glu Ala Ala Arg Glu Cys Arg Arg Lys Lys Lys Glu Tyr Val Lys Cys
225 230 235 240

Leu Glu Asn Arg Val Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile
245 250 255

Glu Glu Leu Lys Thr Leu Lys Asp Leu Tyr Ser Asn Lys Ser Val
260 265 270

<210> 2
<211> 341
<212> PRT
<213> Homo sapiens

<400> 2
Met Thr Met Glu Ser Gly Ala Glu Asn Gln Gln Ser Gly Asp Ala Ala
1 5 10 15

Val Thr Glu Ala Glu Asn Gln Gln Met Thr Val Gln Ala Gln Pro Gln
20 25 30

Ile Ala Thr Leu Ala Gln Val Ser Met Pro Ala Ala His Ala Thr Ser
35 40 45

Ser Ala Pro Thr Val Thr Leu Val Gln Leu Pro Asn Gly Gln Thr Val
50 55 60

Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser Val Ile Gln Ser
65 70 75 80

Pro Gln Val Gln Thr Val Gln Ser Ser Cys Lys Asp Leu Lys Arg Leu
85 90 95

Phe Ser Gly Thr Gln Ile Ser Thr Ile Ala Glu Ser Glu Asp Ser Gln
100 105 110

Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Glu Ile Leu
115 120 125

Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Asp Leu Ser Ser Asp
130 135 140

Ala Pro Gly Val Pro Arg Ile Glu Glu Glu Lys Ser Glu Glu Glu Thr
145 150 155 160

Ser Ala Pro Ala Ile Thr Thr Val Thr Val Pro Thr Pro Ile Tyr Gln
165 170 175

Thr Ser Ser Gly Gln Tyr Ile Ala Ile Thr Gln Gly Gly Ala Ile Gln
180 185 190

Leu Ala Asn Asn Gly Thr Asp Gly Val Gln Gly Leu Gln Thr Leu Thr
195 200 205

Met Thr Asn Ala Ala Ala Thr Gln Pro Gly Thr Thr Ile Leu Gln Tyr
210 215 220

Ala Gln Thr Thr Asp Gly Gln Gln Ile Leu Val Pro Ser Asn Gln Val
225 230 235 240

Val Val Gln Ala Ala Ser Gly Asp Val Gln Thr Tyr Gln Ile Arg Thr
245 250 255

Ala Pro Thr Ser Thr Ile Ala Pro Gly Val Val Met Ala Ser Ser Pro
260 265 270

Ala Leu Pro Thr Gln Pro Ala Glu Glu Ala Ala Arg Lys Arg Glu Val
275 280 285

Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu Cys Arg Arg Lys Lys
290 295 300

Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val Ala Val Leu Glu Asn
305 310 315 320

Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala Leu Lys Asp Leu Tyr
325 330 335

Cys His Lys Ser Asp
340

<210> 3
<211> 281
<212> PRT
<213> Saccharomyces cerevisiae

<400> 3
Met Ser Glu Tyr Gln Pro Ser Leu Phe Ala Leu Asn Pro Met Gly Phe
1 5 10 15

Ser Pro Leu Asp Gly Ser Lys Ser Thr Asn Glu Asn Val Ser Ala Ser
20 25 30

Thr Ser Thr Ala Lys Pro Met Val Gly Gln Leu Ile Phe Asp Lys Phe
35 40 45

Ile Lys Thr Glu Glu Asp Pro Ile Ile Lys Gln Asp Thr Pro Ser Asn
50 55 60

Leu Asp Phe Asp Phe Ala Leu Pro Gln Thr Ala Thr Ala Pro Asp Ala
65 70 75 80

Lys Thr Val Leu Pro Ile Pro Glu Leu Asp Asp Ala Val Val Glu Ser
85 90 95

Phe Phe Ser Ser Ser Thr Asp Ser Thr Pro Met Phe Glu Tyr Glu Asn
100 105 110

Leu Glu Asp Asn Ser Lys Glu Trp Thr Ser Leu Phe Asp Asn Asp Ile
115 120 125

Pro Val Thr Thr Asp Asp Val Ser Leu Ala Asp Lys Ala Ile Glu Ser
130 135 140

Thr Glu Glu Val Ser Leu Val Pro Ser Asn Leu Glu Val Ser Thr Thr
145 150 155 160

Ser Phe Leu Pro Thr Pro Val Leu Glu Asp Ala Lys Leu Thr Gln Thr
165 170 175

Arg Lys Val Lys Lys Pro Asn Ser Val Val Lys Lys Ser His His Val
180 185 190

Gly Lys Asp Asp Glu Ser Arg Leu Asp His Leu Gly Val Val Ala Tyr
195 200 205

Asn Arg Lys Gln Arg Ser Ile Pro Leu Ser Pro Ile Val Pro Glu Ile
210 215 220

Asp Asp Pro Ala Ala Leu Lys Arg Ala Arg Asn Thr Glu Ala Ala Arg
225 230 235 240

Arg Ser Arg Ala Arg Lys Leu Gln Arg Met Lys Gln Leu Glu Asp Lys
245 250 255

Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val Ala
260 265 270

Arg Leu Lys Lys Leu Val Gly Glu Arg
275 280

<210> 4

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 4

agagattgcc tgacgtcaga gagctag

27

<210> 5

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 5

cgcttgatga gtcagccgga a

21

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 6

gactagatga gagctactct aagaggaacg

30

<210> 7

<211> 94

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Protein

<400> 7

Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Trp Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Glu
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val
35 40 45

Ala Tyr Ile Ser Ser Gly Ser Ser Thr Leu His Tyr Ala Asp Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Pro Lys Asn Thr Leu Phe
65 70 75 80

Leu Gln Met Lys Leu Pro Ser Leu Cys Tyr Gly Leu Leu Gly
85 90

<210> 8

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Protein

<400> 8

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
 1 5 10 15
 Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met
 20 25 30
 Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Phe
 35 40 45
 Gly Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Thr Gly Ser
 50 55 60
 Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu
 65 70 75 80
 Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Phe Thr
 85 90 95
 Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

<210> 9
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Peptide
 Internal Fragment

<400> 9
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 10
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Peptide

<220>
 <221> SITE
 <222> (1)
 <223> This is an acidic amino acid.

<220>
 <221> SITE
 <222> (2)
 <223> This is an acidic amino acid.

<220>
 <221> SITE
 <222> (3)..(5)

<223> This amino acid is either leucine or arginine.

<223> Positions 9-10 represent a total of 1 or 2 amino acid residues and these can be any amino acid residues.

10

<213> Artificial Sequence

<223> Description of Artificial Sequence: Peptide

<223> Positions 1-5 represent a total of 1, 2, 3, 4 or 5 amino acid residues and these can be any amino acid residues.

<223> Residues 6 and 7 are acidic amino acid residues.

<223> Positions 8-10 represent a total of 2 or 3 amino acid residues and these can be any amino acid residues.

<223> This amino acid residue is either leucine or arginine.

<222> (14) .. (15)

<223> Positions 14-15 represent a total of either 1 or 2 amino acid residues and these can be any amino acid residues.

<220>

<221> SITE

<222> (17)..(19)

<223> Positions 17-19 represent a total of 0, 1, 2 or 3 amino acid residues and these can be any amino acid residues.

<400> 11

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Arg Xaa Xaa Arg
1 5 10 15

Xaa Xaa Xaa Asn
20

<210> 12

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

<220>

<221> SITE

<222> (1)..(5)

<223> Positions 1-5 represent a total of 1, 2, 3, 4 or 5 amino acid residues and these can be any amino acid residues.

<220>

<221> SITE

<222> (6)..(7)

<223> Positions 6 and 7 represent acidic amino acid residues.

<220>

<221> SITE

<222> (8)..(10)

<223> Positions 8-10 represent a total of 2 or 3 amino acid residues and these can be any amino acid residues.

<220>

<221> SITE

<222> (11)

<223> Position 11 is either leucine or arginine.

<220>

<221> SITE

<222> (14)..(15)

<223> Positions 14-15 represent a total of 1 or 2 amino acid residues and these can be any amino acid

residues.

<220>
 <221> SITE
 <222> (17)..(19)
 <223> Positions 17-19 represent a total of 0, 1, 2 or 3
 amino acid residues and these can be any amino
 acid residues.

<220>
 <221> SITE
 <222> (21)
 <223> This can be any amino acid residue.

<220>
 <221> SITE
 <222> (22)
 <223> Position 22 represents glutamic acid-alanine.

<220>
 <221> SITE
 <222> (25)
 <223> Position 25 represents glutamic acid-alanine.

<220>
 <221> SITE
 <222> (28)..(31)
 <223> Positions 28-31 represent a total of 3 or 4 amino
 acid residues and these can be any amino acid
 residues.

<400> 12
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Arg Xaa Xaa Arg
 1 5 10 15
 Xaa Xaa Xaa Asn Xaa Xaa Ala Arg Xaa Arg Lys Xaa Xaa Xaa Xaa
 20 25 30

<210> 13
 <211> 14
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<400> 13
 gcctgacgtc accg